

Chaotic Dynamics Can Generate Macroecological Laws in Microbiota

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Recent works identified quantitative relationships in the dynamics of bacterial taxonomic composition that are consistent with known relationships in macroecological systems. However, quantitative mechanisms that generate these dynamics have not been fully characterized. Understanding these mechanisms is important for answering long-standing questions in quantitative ecology. Here we present a model that accurately reproduces ecological dynamics in the human gut microbiota. The model provides several key insights into the origins of the variability of species abundances in ecology.

I. BACKGROUND

THE human gut microbiota consists of hundreds of bacterial species, and bacterial composition varies significantly between individuals [1], in terms of time [2-4], and spatially within the gut [5]. We and others have previously shown that the dynamics of the gut microbiota are characterized by the same quantitative scaling laws as those observed in ecology of plants and animals [6-7].

Although various mathematical models exist in ecology that aim to explain the origins of individual scaling laws in animal and plant species [8-9], the nature of these laws remains an open area of research [9]. More recent models of microbiota also stop short of reproducing all known statistical scaling laws with the correct scaling coefficients [10-11]. We believe that in order to gain meaningful insights into open questions in mathematical ecology, such as the relationship between biodiversity and stability [12], a model that can capture all ecological scaling laws with accurate coefficients is currently necessary.

II. RESULTS

We developed a generalized Lotka-Volterra model of gut microbial dynamics, which was able to accurately reproduce all considered scaling laws in microbiota. Our model possesses several conceptually important features.

A. No environmental stochasticity

Environmental stochasticity is not required for maintaining the necessary temporal dynamics on short time scales. By implementing a model without external sources of noise, we seek to assess whether deterministic chaos can reproduce abundance profiles with low short-term autocorrelation that have been observed in nature, without assuming that environmental fluctuations or measurement noise are the primary culprits of this behavior.

B. Spatial heterogeneity

We incorporate spatial variability into the model, which results in long-term stability. Explicit modeling of spatial structure provides our analysis with an additional level of interpretability, allowing comparisons with experimental spatial microbiota measurements, such as DIVERS [5].

C. Carrying capacities and total load

Our model does not require predetermined fixed carrying capacities for each species. Instead, the rank-abundance population structure arises naturally as an emergent property of the dynamic system. Finally, although measurements of the ecological state of the system are performed on normalized, compositional data, our model explicitly accounts for variability in total abundances of all species.

III. CONCLUSION

We present a model of microbiota that, for the first time, is able to reproduce all considered ecological scaling laws with accurate coefficients. The assumptions of the model, and subsequent analyses, give several key insights into the mathematical mechanisms required for generating realistic ecological systems.

REFERENCES

- [1] Human Microbiome Project Consortium. (2012). Structure, function and diversity of the healthy human microbiome. *Nature*, 486(7402), 207.
- [2] Caporaso, J. G., et al. (2011). Moving pictures of the human microbiome. *Genome biology*, 12(5), 1-8.
- [3] David, L. A., et al. (2014). Host lifestyle affects human microbiota on daily timescales. *Genome biology*, 15(7), 1-15.
- [4] Faith, J. J., et al. (2013). The long-term stability of the human gut microbiota. *Science*, 341(6141), 1237439.
- [5] Ji, B. W., et al. (2019). Quantifying spatiotemporal variability and noise in absolute microbiota abundances using replicate sampling. *Nature methods*, 16(8), 731-736.
- [6] Ji, B. W., et al. (2020). Macroecological dynamics of gut microbiota. *Nature microbiology*, 5(5), 768-775.
- [7] Grilli, J. (2020). Macroecological laws describe variation and diversity in microbial communities. *Nature communications*, 11(1), 1-11.
- [8] Taylor, L. R., & Taylor, R. A. J. (1977). Aggregation, migration and population mechanics. *Nature*, 265(5593), 415-421.
- [9] Eisler, Z., et al. (2008). Fluctuation scaling in complex systems: Taylor's law and beyond. *Advances in Physics*, 57(1), 89-142.
- [10] Zaoli, S., & Grilli, J. (2021). A macroecological description of alternative stable states reproduces intra- and inter-host variability of gut microbiome. *Science Advances*, 7(43), eabj2882.
- [11] Ho, P. Y., Good, B., & Huang, K. C. (2021). Competition for fluctuating resources reproduces statistics of species abundance over time across wide-ranging microbiotas. *bioRxiv*.
- [12] Ratzke, C., Barrere, J., & Gore, J. (2020). Strength of species interactions determines biodiversity and stability in microbial communities. *Nature ecology & evolution*, 4(3), 376-383.

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